

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: The Regents of the University of California
- (ii) TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Robbins, Berliner & Carson
 - (B) STREET: 201 N. Figueroa Street, 5th Floor
 - (C) CITY: Los Angeles
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 90012-2628
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Berliner, Robert
 - (B) REGISTRATION NUMBER: 20,121
 - (C) REFERENCE/DOCKET NUMBER: 5555-291
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 310-977-1001
 - (B) TELEFAX: 310-977-1003
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 40..1161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT | 54 |
| Met Leu Ser Thr Ser | |
| 1 5 | |
| CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC | 102 |
| Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr | |
| 10 15 20 | |
| ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG | 150 |
| Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val | |
| 25 30 35 | |
| AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC | 198 |
| Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe | |
| 40 45 50 | |
| ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC | 246 |
| Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn | |
| 55 60 65 | |
| TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC | 294 |
| Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala | |
| 70 75 80 85 | |
| ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT | 342 |
| Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser | |
| 90 95 100 | |

| | |
|---|-----|
| GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr 105 110 115 | 390 |
| GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu 120 125 130 | 438 |
| CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu 135 140 145 | 486 |
| AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp 150 155 160 165 | 534 |
| TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys 170 175 180 | 582 |
| CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly 185 190 195 | 630 |
| TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu 200 205 210 | 678 |
| CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu 215 220 225 | 726 |
| CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile 230 235 240 245 | 774 |
| TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile 250 255 260 | 822 |
| GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys 265 270 275 | 870 |
| GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu 280 285 290 | 918 |

| | |
|--|------|
| GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG | 966 |
| Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly | |
| 295 300 305 | |
| GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC | 1014 |
| Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala | |
| 310 315 320 325 | |
| CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG | 1062 |
| Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys | |
| 330 335 340 | |
| AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA | 1110 |
| Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly | |
| 345 350 355 | |
| AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA | 1158 |
| Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly | |
| 360 365 370 | |
| GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC | 1211 |
| Ala | |
| ACAGATGTGT GATTACAGT GTGAATCTTG GTGTCTACGT TACCAGGCAG GAAGGCTGAG | 1271 |
| AGGAGAGAGA CTCCAGCTGG GTTGGA AAC AGTATTTTCC AAACCTACCTT CCAGTTCCTC | 1331 |
| ATTTTGAAT ACAGGCATAG AGTTCAGACT TTTTAAAT AGTAAAAATA AAATTAAAGC | 1391 |
| TGAAAACCTGC AACTTGTAAG TGTGGTAAAG AGTTAGTTTG AGTTGCTATC ATGTCAAACG | 1451 |
| TGAAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG | 1511 |
| GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA | 1571 |
| GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT | 1631 |
| TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTC TCTCAGGCTT | 1691 |
| GCTGCCAAAA GCCTTTTGTG TTTTGTGTTG TATCATTATG AAGTCATGCG TTAAATCACA | 1751 |
| TTGAGTGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTGGCCA | 1811 |
| GTGGGAACCTC CTAAATCAAA TTGGCTTCTA ATCAAAGCTT TTAACCCCTA TTGGTAAAGA | 1871 |
| ATGGAAGGTG GAGAAGCTCG CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT | 1931 |
| AAGAATGTTT TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC | 1991 |

TTCTAGAACC AGGCAACTTG GGAAGTAGAC TCCCAAGCTG GACTATGGCT CTACTTTCAG 2051
 GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA 2111
 TATATTTGTA TGATCCTAAT GAATGCATAA AATGTAAAGT TGATGGTGAT GAAATGTAAA 2171
 TACTGTTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA 2231
 G 2232

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Thr | Ser | Arg | Ser | Arg | Phe | Ile | Arg | Asn | Thr | Asn | Glu | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Glu | Glu | Val | Thr | Thr | Phe | Phe | Asp | Tyr | Asp | Tyr | Gly | Ala | Pro | Cys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Lys | Phe | Asp | Val | Lys | Gln | Ile | Gly | Ala | Gln | Leu | Leu | Pro | Pro | Leu |
| | | | 35 | | | | 40 | | | | 45 | | | | |
| Tyr | Ser | Leu | Val | Phe | Ile | Phe | Gly | Phe | Val | Gly | Asn | Met | Leu | Val | Val |
| | | 50 | | | | 55 | | | | 60 | | | | | |
| Leu | Ile | Leu | Ile | Asn | Cys | Lys | Lys | Leu | Lys | Cys | Leu | Thr | Asp | Ile | Tyr |
| 65 | | | | 70 | | | | 75 | | | 80 | | | | |
| Leu | Leu | Asn | Leu | Ala | Ile | Ser | Asp | Leu | Leu | Phe | Leu | Ile | Thr | Leu | Pro |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Leu | Trp | Ala | His | Ser | Ala | Ala | Asn | Glu | Trp | Val | Phe | Gly | Asn | Ala | Met |
| | | | 100 | | | | 105 | | | | | 110 | | | |
| Cys | Lys | Leu | Phe | Thr | Gly | Leu | Tyr | His | Ile | Gly | Tyr | Phe | Gly | Gly | Ile |
| | | 115 | | | | 120 | | | | | 125 | | | | |
| Phe | Phe | Ile | Ile | Leu | Leu | Thr | Ile | Asp | Arg | Tyr | Leu | Ala | Ile | Val | His |
| | | 130 | | | | 135 | | | | | 140 | | | | |

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
180 185 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
195 200 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
210 215 220

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
260 265 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
275 280 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
290 295 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
305 310 315 320

Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
325 330 335

Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
340 345 350

Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
355 360 365

Gln Asp Lys Glu Gly Ala
370

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1979 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 81..1160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----|
| CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT | 60 |
| TTCCCCAGTA CATCCACAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC | 110 |
| Met Leu Ser Thr Ser Arg Ser Arg Phe Ile | |
| 1 5 10 | |
| AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT | 158 |
| Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr | |
| 15 20 25 | |
| GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC | 206 |
| Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala | |
| 30 35 40 | |
| CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG | 254 |
| Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val | |
| 45 50 55 | |
| GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG | 302 |
| Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys | |
| 60 65 70 | |
| TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT | 350 |
| Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu | |
| 75 80 85 90 | |
| TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG | 398 |
| Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp | |
| 95 100 105 | |

| | |
|---|-----|
| GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile 110 115 120 | 446 |
| GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg 125 130 135 | 494 |
| TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val 140 145 150 | 542 |
| ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val Ala Val Phe 155 160 165 170 | 590 |
| GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC CAG AAA GAA GAT TCT Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser 175 180 185 | 638 |
| GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA TGG AAT AAT TTC CAC Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly Trp Asn Asn Phe His 190 195 200 | 686 |
| ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG CCG CTG CTC ATC ATG Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu Pro Leu Leu Ile Met 205 210 215 | 734 |
| GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG CTT CGG TGT CGA AAC Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn 220 225 230 | 782 |
| GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC TTC ACC ATC ATG ATT Glu Lys Lys Arg His Arg Ala Val Arg Val Ile Phe Thr Ile Met Ile 235 240 245 250 | 830 |
| GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT GTC ATT CTC CTG AAC Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn 255 260 265 | 878 |
| ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT GAA AGC ACC AGT CAA Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln 270 275 280 | 926 |
| CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT GGG ATG ACT CAC TGC Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu Gly Met Thr His Cys 285 290 295 | 974 |

| | |
|---|------|
| TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG GAG AAG TTC AGA AGG Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg 300 305 310 | 1022 |
| TAT CTC TCG GTG TTC TTC CGA AAG CAC ATC ACC AAG CGC TTC TGC AAA Tyr Leu Ser Val Phe Phe Arg Lys His Ile Thr Lys Arg Phe Cys Lys 315 320 325 330 | 1070 |
| CAA TGT CCA GTT TTC TAC AGG GAG ACA GTG GAT GGA GTG ACT TCA ACA Gln Cys Pro Val Phe Tyr Arg Glu Thr Val Asp Gly Val Thr Ser Thr 335 340 345 | 1118 |
| AAC ACG CCT TCC ACT GGG GAG CAG GAA GTC TCG GCT GGT TTA Asn Thr Pro Ser Thr Gly Glu Gln Glu Val Ser Ala Gly Leu 350 355 360 | 1160 |
| TAAAACGAGG AGCAGTTTGA TTGTTGTTTA TAAAGGGAGA TAACAATCTG TATATAACAA | 1220 |
| CAAACTTCAA GGGTTTGTG AACAAATAGAA ACCTGTAAAG CAGGTGCCCA GGAACCTCAG | 1280 |
| GGCTGTGTGT ACTAATACAG ACTATGTCAC CCAATGCATA TCCAACATGT GCTCAGGGAA | 1340 |
| TAATCCAGAA AACTGTGGG TAGAGACTTT GACTCTCCAG AAAGCTCATC TCAGCTCCTG | 1400 |
| AAAAATGCCT CATTACCTTG TGCTAATCCT CTTTTTCTAG TCTTCATAAT TTCTTCACTC | 1460 |
| AATCTCTGAT TCTGTCAATG TCTTGAAATC AAGGGCCAGC TGGAGGTGAA GAAGAGAATG | 1520 |
| TGACAGGCAC AGATGAATGG GAGTGAGGGA TAGTGGGGTC AGGGCTGAGA GGAGAAGGAG | 1580 |
| GGAGACATGA GCATGGCTGA GCCTGGACAA AGACAAAGGT GAGCAAAGGG CTCACGCATT | 1640 |
| CAGCCAGGAG ATGATACTGG TCCTTAGCCC CATCTGCCAC GTGTATTTAA CCTTGAAGGG | 1700 |
| TTCACCAGGT CAGGGAGAGT TTGGGAACTG CAATAACCTG GGAGTTTTGG TGGAGTCCGA | 1760 |
| TGATTCTCTT TTGCATAAGT GCATGACATA TTTTGTCTT ATTACAGTT ATCTATGGCA | 1820 |
| CCCATGCACC TTACATTTGA AATCTATGAA ATATCATGCT CCATTGTTCA GATGCTTCTT | 1880 |
| AGGCCACATC CCCCTGTCTA AAAATTCAGA AAATTTTGT TTATAAAAGA TGCATTATCT | 1940 |
| ATGATATGCT AATATATGTA TATGCAATAT AAAATTTAG | 1979 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Thr | Ser | Arg | Ser | Arg | Phe | Ile | Arg | Asn | Thr | Asn | Glu | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Glu | Glu | Val | Thr | Thr | Phe | Phe | Asp | Tyr | Asp | Tyr | Gly | Ala | Pro | Cys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Lys | Phe | Asp | Val | Lys | Gln | Ile | Gly | Ala | Gln | Leu | Leu | Pro | Pro | Leu |
| | | 35 | | | | | 40 | | | | 45 | | | | |
| Tyr | Ser | Leu | Val | Phe | Ile | Phe | Gly | Phe | Val | Gly | Asn | Met | Leu | Val | Val |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Leu | Ile | Leu | Ile | Asn | Cys | Lys | Lys | Leu | Lys | Cys | Leu | Thr | Asp | Ile | Tyr |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Leu | Asn | Leu | Ala | Ile | Ser | Asp | Leu | Leu | Phe | Leu | Ile | Thr | Leu | Pro |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Leu | Trp | Ala | His | Ser | Ala | Ala | Asn | Glu | Trp | Val | Phe | Gly | Asn | Ala | Met |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Cys | Lys | Leu | Phe | Thr | Gly | Leu | Tyr | His | Ile | Gly | Tyr | Phe | Gly | Gly | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Phe | Phe | Ile | Ile | Leu | Leu | Thr | Ile | Asp | Arg | Tyr | Leu | Ala | Ile | Val | His |
| | 130 | | | | | 135 | | | | | | 140 | | | |
| Ala | Val | Phe | Ala | Leu | Lys | Ala | Arg | Thr | Val | Thr | Phe | Gly | Val | Val | Thr |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Ser | Val | Ile | Thr | Trp | Leu | Val | Ala | Val | Phe | Ala | Ser | Val | Pro | Gly | Ile |
| | | | 165 | | | | 170 | | | | | 175 | | | |
| Ile | Phe | Thr | Lys | Cys | Gln | Lys | Glu | Asp | Ser | Val | Tyr | Val | Cys | Gly | Pro |
| | | 180 | | | | | 185 | | | | | 190 | | | |
| Tyr | Phe | Pro | Arg | Gly | Trp | Asn | Asn | Phe | His | Thr | Ile | Met | Arg | Asn | Ile |
| | | 195 | | | | | 200 | | | | | 205 | | | |

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220
 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240
 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255
 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270
 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285
 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300
 Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Leu Ser Val Phe Phe
 305 310 315 320
 Arg Lys His Ile Thr Lys Arg Phe Cys Lys Gln Cys Pro Val Phe Tyr
 325 330 335
 Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly
 340 345 350
 Glu Gln Glu Val Ser Ala Gly Leu
 355 360

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
 1 5 10 15

Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
 20 25 30
 Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
 35 40 45
 Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
 50 55 60
 Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80
 Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
 85 90 95
 Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
 100 105 110
 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
 115 120 125
 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
 130 135 140
 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
 145 150 155 160
 Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
 165 170 175
 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
 180 185 190
 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
 195 200 205
 Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220
 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
 225 230 235 240
 Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn
 245 250 255
 Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
 260 265 270

Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
 275 280 285

Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
 290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
 305 310 315 320

Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
 325 330 335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser
 340 345 350

Ala Gly Phe
 355

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
 1 5 10 15

Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
 20 25 30

Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Tyr Ile Tyr Ser Ile Ile
 35 40 45

Phe Leu Tyr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
 50 55 60

Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
 65 70 75 80

| | | | |
|---|-----|-----|-----|
| Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val | | | |
| 85 | 90 | 95 | |
| Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val | | | |
| 100 | 105 | 110 | |
| His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala | | | |
| 115 | 120 | 125 | |
| Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser | | | |
| 130 | 135 | 140 | |
| Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val | | | |
| 145 | 150 | 155 | 160 |
| Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn | | | |
| 165 | 170 | 175 | |
| Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn | | | |
| 180 | 185 | 190 | |
| Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu | | | |
| 195 | 200 | 205 | |
| Ile Leu Pro Gly Ile Val Ile Leu Phe Cys Tyr Cys Ile Ile Ile Ser | | | |
| 210 | 215 | 220 | |
| Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Tyr | | | |
| 225 | 230 | 235 | 240 |
| Tyr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr | | | |
| 245 | 250 | 255 | |
| Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln | | | |
| 260 | 265 | 270 | |
| Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu | | | |
| 275 | 280 | 285 | |
| Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe | | | |
| 290 | 295 | 300 | |
| Leu Gly Ala Lys Phe Lys Tyr Ser Ala Gln His Ala Leu Thr Ser Val | | | |
| 305 | 310 | 315 | 320 |
| Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly | | | |
| 325 | 330 | 335 | |

His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
340 345 350

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe Asp Asp Leu Asn
1 5 10 15

Phe Thr Gly Met Pro Pro Ala Asp Glu Asp Tyr Ser Pro Cys Met Leu
20 25 30

Glu Thr Glu Thr Leu Asn Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu
35 40 45

Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met Leu Val Ile
50 55 60

Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr Leu Leu Asn
65 70 75 80

Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro Ile Trp Ala
85 90 95

Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu Cys Lys Val
100 105 110

Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu Leu Leu
115 120 125

Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His Ala Thr Arg
130 135 140

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Thr | Gln | Lys | Arg | His | Leu | Val | Lys | Phe | Val | Cys | Leu | Gly | Cys |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Trp | Gly | Leu | Ser | Met | Asn | Leu | Ser | Leu | Pro | Phe | Phe | Leu | Phe | Arg | Gln |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Ala | Tyr | His | Pro | Asn | Asn | Ser | Ser | Pro | Val | Cys | Tyr | Glu | Val | Leu | Gly |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Asn | Asp | Thr | Ala | Lys | Trp | Arg | Met | Val | Leu | Arg | Ile | Leu | Pro | His | Thr |
| | 195 | | | | | | 200 | | | | 205 | | | | |
| Phe | Gly | Phe | Ile | Val | Pro | Leu | Phe | Val | Met | Leu | Phe | Cys | Tyr | Gly | Phe |
| 210 | | | | | | 215 | | | | | 220 | | | | |
| Thr | Leu | Arg | Thr | Leu | Phe | Lys | Ala | His | Met | Gly | Gln | Lys | His | Arg | Ala |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Met | Arg | Val | Ile | Phe | Ala | Val | Val | Leu | Ile | Phe | Leu | Leu | Cys | Trp | Leu |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Pro | Tyr | Asn | Leu | Val | Leu | Leu | Ala | Asp | Thr | Leu | Met | Arg | Thr | Gln | Val |
| | | 260 | | | | | | | 265 | | | | | 270 | |
| Ile | Gln | Glu | Thr | Cys | Glu | Arg | Arg | Asn | Asn | Ile | Gly | Arg | Ala | Leu | Asp |
| | 275 | | | | | | | 280 | | | | 285 | | | |
| Ala | Thr | Glu | Ile | Leu | Gly | Phe | Leu | His | Ser | Cys | Leu | Asn | Pro | Ile | Ile |
| | 290 | | | | | | 295 | | | | | 300 | | | |
| Tyr | Ala | Phe | Ile | Gly | Gln | Asn | Phe | Arg | His | Gly | Phe | Leu | Lys | Ile | Leu |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ala | Met | His | Gly | Leu | Val | Ser | Lys | Glu | Phe | Leu | Ala | Arg | His | Arg | Val |
| | | | 325 | | | | | | 330 | | | | | 335 | |
| Thr | Ser | Tyr | Thr | Ser | Ser | Ser | Val | Asn | Val | Ser | Ser | Asn | Leu | | |
| | | 340 | | | | | | 345 | | | | 350 | | | |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser
1 5 10 15

Asn Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala
20 25 30

Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile
35 40 45

Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val
50 55 60

Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val
65 70 75 80

Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu
85 90 95

Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe
100 105 110

Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly
115 120 125

Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val
130 135 140

His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile
145 150 155 160

Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu
165 170 175

Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr
180 185 190

Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile
195 200 205

Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe
210 215 220

Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln
225 230 235 240

Lys His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu
 245 250 255
 Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met
 260 265 270
 Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn His Ile Asp
 275 280 285
 Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu
 290 295 300
 Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu
 305 310 315 320
 Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro
 325 330 335
 Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser
 340 345 350
 Thr Thr Leu
 355

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCTCGAGAC CTRKCHDTKK CYGACCT

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGAATTCTG GACRATGGCC AGGTAVCKGT C

31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Leu Ala Ile Ser Asp Leu

1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Arg Tyr Leu Ala Ile Val

1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Phe | Phe | Ile | Ile | Leu | Leu | Thr | Ile | Asp | Arg | Tyr | Leu | Ala | Ile | Val |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| His | Ala | Val | Phe | Ala | Leu | Lys | Ala | Arg | Thr | Val | Thr | Phe | Gly | Val | |
| | | | 20 | | | | | 25 | | | | | | 30 | |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Phe | Phe | Ile | Ile | Leu | Leu | Thr | Ile | Asp | Arg | Tyr | Leu | Ala | Ile | Val |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| His | Ala | Val | Phe | Ala | Leu | Arg | Ala | Arg | Thr | Val | Thr | Phe | Gly | Val | |
| | | | 20 | | | | | 25 | | | | | | 30 | |